AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-37 (Cancelled)

38. (Currently amended) A protein variant which substitutes a valine residue for a phenylalanine residue in a binding domain of a 4-alpha helix bundle cytokine selected from the group consisting of CNTF, EPO, F1t3L, G-CSF, GM-CSF, GH, IL-2, IL-3, IL-4, 1L-5, IL-6, IL-12p35, LPT, LIF, M-CSF, OSM, PL, SCF, TPO, IFN-α2A, IFN-α2B, IFN-β IFN-γ, IPN-ω and IFN-τ.

39-40 (Cancelled)

41. (Currently amended) The protein variant according to claim 38[[40]], wherein: ~~the 4-alpha helix bundle cytokine is selected from the group consisting of CNTF, EPO, F1t3L, G-CSF, GM-CSF, GH, IL-2, IL-3, IL-4, 1L-5, IL-6, IL-12p35, LPT, LIF, M-CSF, OSM, PL, SCF, TPO, IFN-α2A, IFN-α2B, IFN-β IFN-γ, IPN-ω and IFN-τ.~~

- the CNTF, EPO, F1t3L, G-CSF, GH, IL-4, IL-6, IL-12p35, LPT, LIF, OSM, PL, and TPO are wild-type and are altered by substituting a valine residue for a phenylalanine residue of amino acid residues between positions 110 to 180; and

- the IFN-α2A, IFN-α2B, IFN-β, IFN-γ, IFN-ω and IFN-τ are wild-type and are altered by substituting a valine residue for a phenylalanine residue of amino acid residues between positions 1 to 50.

42. (Currently Amended) The protein variant according to claim 41, wherein: ~~the CNTF, EPO, F1t3L, G-CSF, GM-CSF, GH, IL-2, IL-3, IL4, 1L-5, M-6, IL-12p35, LPT, L1F, M-CSF, OSM, PL, SCF and TPO are altered by substituting a valine for at least one phenylalanine residue within the amino acid residues in a binding domain having the sequence of amino acid residues between positions 110 and 180 of SEQ ID NO.: 25.~~

- the CNTF is altered by substituting a valine residue for a phenylalanine residue at

position 119, 152 or 178 of an amino acid sequence designed as SEQ ID NO.:1;

- the EPO is altered by substituting a valine residue for a phenylalanine residue at position 138, 142 or 148 of an amino acid sequence designed as SEQ ID NO.:2;

- the G-CSF is altered by substituting a valine residue for a phenylalanine residue at position 116, 143, 147 or 163 of an amino acid sequence designed as SEQ ID NO.:4;

- the GM-CSF is altered by substituting a valine residue for a phenylalanine residue at position 103, 106, 113 or 119 of an amino acid sequence designed as SEQ ID NO.:5;

- the GH is altered by substituting a valine residue for a phenylalanine residue at position 139, 146, 166, 176 or 191 of an amino acid sequence designed as SEQ ID NO.:6;

- the IL-2 is altered by substituting a valine residue for a phenylalanine residue at position 42 or 44 of an amino acid sequence designed as SEQ ID NO.:13;

- the IL-3 is altered by substituting a valine residue for a phenylalanine residue at position 107 or 113 of an amino acid sequence designed as SEQ ID NO.:14;

- the IL-4 is altered by substituting a valine residue for a phenylalanine residue at position 112 of an amino acid sequence designed as SEQ ID NO.:15;

- the IL-5 is altered by substituting a valine residue for a phenylalanine residue at position 69 of an amino acid sequence designed as SEQ ID NO.:16;

- the IL-6 is altered by substituting a valine residue for a phenylalanine residue at position 124 of an amino acid sequence designed as SEQ ID NO.:17;

- the IL-12p35 is altered by substituting a valine residue for a phenylalanine residue at position 180 of an amino acid sequence designed as SEQ ID NO.:18;

- the LPT is altered by substituting a valine residue for a phenylalanine residue at position 41 or 92 of an amino acid sequence designed as SEQ ID NO.:19;

- the LIF is altered by substituting a valine residue for a phenylalanine residue at position 156 of an amino acid sequence designed as SEQ ID NO.:20;

- the M-CSF is altered by substituting a valine residue for a phenylalanine residue at position 311 of an amino acid sequence designed as SEQ ID NO.:21;

- the OSM is altered by substituting a valine residue for a phenylalanine residue at position 160 or 169 of an amino acid sequence designed as SEQ ID NO.:22;

- the PL is altered by substituting a valine residue for a phenylalanine residue at position 166 or 176 of an amino acid sequence designed as SEQ ID NO.:23;

- the SCF is altered by substituting a valine residue for a phenylalanine residue at position 199, 205 or 207 of an amino acid sequence designed as SEQ ID NO.:24;

- the TPO is altered by substituting a valine residue for a phenylalanine residue at position 131 of an amino acid sequence designed as SEQ ID NO.:25;

- the IFN-α2A is altered by substituting a valine residue for a phenylalanine residue at position 27, 36 or 38 of an amino acid sequence designed as SEQ ID NO.:7;

- the IFN-α2B is altered by substituting a valine residue for a phenylalanine residue at position 27, 36 or 38 of an amino acid sequence designed as SEQ ID NO.:8;

- the IFN-β is altered by substituting a valine residue for a phenylalanine residue at position 38 of an amino acid sequence designed as SEQ ID NO.:9;

- the IFN-γ is altered by substituting a valine residue for a phenylalanine residue at position 32 of an amino acid sequence designed as SEQ ID NO.:10;

- the IFN-ω is altered by substituting a valine residue for a phenylalanine residue at position 27, 36 or 38 of an amino acid sequence designed as SEQ ID NO.:11; and

- the IFN-τ is altered by substituting a valine residue for a phenylalanine residue at position 39 of an amino acid sequence designed as SEQ ID NO.:12.

43-75 (Cancelled)

76. (New) A pharmaceutical composition comprising the protein variant of claim 38 and a pharmaceutically acceptable carrier.

77. (New) A pharmaceutical composition comprising the protein variant of claim 41 and a pharmaceutically acceptable carrier.

78. (New) A pharmaceutical composition comprising the protein variant of claim 42 and a pharmaceutically acceptable carrier.